Sequence List[illegible]

(1) Name of Applicant: Chugai Research Institute for Molecular Medicine, Inc.

(2) Title of the Invention: NOVEL MEMBRANE-SECRETED PROTEIN

(3) Reference Number: C1-806PCT

(4) Application Number:

(5) Filing Date:

(6) Country where the priority application was filed and the application numbe
r of the application: Japan, No. Hei 9-099653

(7) Priority date: April 1, 1997

(8) Number of Sequences: 12

SEQ ID NO: 1:

SEQUENCE LENGTH: 176

TOPOLOGY: liner

MOLECULE TYPE: protein

SEQUENCE DENCRIPTION: SEQ ID NO: 1:

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                  Met Val Thr Phe Ser His Val Ser Ser Leu Ser His
                  -28         -25                 -20
Trp Phe Leu Leu Leu Leu Leu Leu Asn Leu Phe Leu Pro Val Ile Phe
    -15                 -10                 -5
Ala Met Pro Glu Ser Tyr Ser Phe Asn Cys Pro Asp Gly Glu Tyr Gln
 1               5                  10                  15
Ser Asn Asp Val Cys Cys Lys Thr Cys Pro Ser Gly Thr Phe Val Lys
            20                  25                  30
Ala Pro Cys Lys Ile Pro His Thr Gln Gly Gln Cys Glu Lys Cys His
        35                  40                  45
Pro Gly Thr Phe Thr Gly Lys Asp Asn Gly Leu His Asp Cys Glu Leu
    50                  55                  60
Cys Ser Thr Cys Asp Lys Asp Gln Asn Met Val Ala Asp Cys Ser Ala
65                  70                  75                  80
Thr Ser Asp Arg Lys Cys Glu Cys Gln Ile Gly Leu Tyr Tyr Tyr Asp
                85                  90                  95
Pro Lys Phe Pro Glu Ser Cys Arg Pro Cys Thr Lys Cys Pro Gln Gly
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105 110

Ile Pro Val Leu Gln Glu Cys Asn Ser Thr Ala Asn Thr Val Cys Ser
115 120 125

Ser Ser Val Ser Asn Pro Arg Asn Trp Leu Phe Leu Leu Met Leu Ile
130 135 140

Val Phe Cys Ile
145

SEQ ID NO: 2:
SEQUENCE LENGTH: 148
TOPOLOGY: liner
MOLECULE TYPE: protein
SEQUENCE DENCRIPTION: SEQ ID NO: 2:

Ala Met Pro Glu Ser Tyr Ser Phe Asn Cys Pro Asp Gly Glu Tyr Gln
1 5 10 15

Ser Asn Asp Val Cys Cys Lys Thr Cys Pro Ser Gly Thr Phe Val Lys
20 25 30

Ala Pro Cys Lys Ile Pro His Thr Gln Gly Gln Cys Glu Lys Cys His
35 40 45

Pro Gly Thr Phe Thr Gly Lys Asp Asn Gly Leu His Asp Cys Glu Leu
50 55 60

Cys Ser Thr Cys Asp Lys Asp Gln Asn Met Val Ala Asp Cys Ser Ala
65 70 75 80

Thr Ser Asp Arg Lys Cys Glu Cys Gln Ile Gly Leu Tyr Tyr Tyr Asp
85 90 95

Pro Lys Phe Pro Glu Ser Cys Arg Pro Cys Thr Lys Cys Pro Gln Gly
100 105 110

Ile Pro Val Leu Gln Glu Cys Asn Ser Thr Ala Asn Thr Val Cys Ser
115 120 125

Ser Ser Val Ser Asn Pro Arg Asn Trp Leu Phe Leu Leu Met Leu Ile
130 135 140

Val Phe Cys Ile
145

SEQ ID NO: 3:
SEQUENCE LENGTH: 1509

STRANDEDNESS: double
TOPOLOGY: liner
MOLECULE TYPE: cDNA to mRNA

FEATURE:
NAME/KEY: CDS
LOCATION: 12..542
IDENTIFICATION: E

NAME/KEY: sig peptide
LOCATION: 12..95
IDENTIFICATION: S

NAME/KEY: mat peptide
LOCATION: 96..542
IDENTIFICATION: S

SEQUENCE DENCRIPTION: SEQ ID NO: 3:

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AGCTCACAGC C ATG GTT ACC TTC AGC CAC GTC TCC AGT CTG AGT CAC          47
                Met Val Thr Phe Ser His Val Ser Ser Leu Ser His
                -28         -25                 -20
TGG TTC CTC TTG CTG CTG CTG CTG AAT CTG TTC TTG CCG GTA ATA TTT        95
Trp Phe Leu Leu Leu Leu Leu Leu Asn Leu Phe Leu Pro Val Ile Phe
    -15                 -10                 -5
GCT ATG CCT GAA TCA TAC TCC TTC AAC TGT CCC GAT GGT GAA TAC CAG       143
Ala Met Pro Glu Ser Tyr Ser Phe Asn Cys Pro Asp Gly Glu Tyr Gln
 1              5                  10                  15
TCT AAT GAT GTC TGT TGC AAG ACC TGT CCC TCA GGT ACA TTT GTC AAG       191
Ser Asn Asp Val Cys Cys Lys Thr Cys Pro Ser Gly Thr Phe Val Lys
            20                  25                  30
GCG CCC TGC AAA ATC CCC CAT ACT CAA GGA CAA TGT GAG AAG TGT CAC       239
Ala Pro Cys Lys Ile Pro His Thr Gln Gly Gln Cys Glu Lys Cys His
        35                  40                  45
CCA GGA ACA TTC ACA GGG AAA GAT AAT GGC CTG CAT GAT TGT GAA CTT       287
Pro Gly Thr Phe Thr Gly Lys Asp Asn Gly Leu His Asp Cys Glu Leu
    50                  55                  60
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TGC TCC ACC TGT GAT AAA GAC CAG AAT ATG GTG GCT GAC TGT TCT GCC          335
Cys Ser Thr Cys Asp Lys Asp Gln Asn Met Val Ala Asp Cys Ser Ala
 65                  70                  75                  80
ACC AGT GAC CGG AAA TGC GAG TGC CAA ATA GGT CTT TAC TAC TAT GAC          383
Thr Ser Asp Arg Lys Cys Glu Cys Gln Ile Gly Leu Tyr Tyr Tyr Asp
                 85                  90                  95
CCA AAA TTT CCG GAA TCA TGC CGC CCA TGT ACC AAG TGT CCC CAA GGA          431
Pro Lys Phe Pro Glu Ser Cys Arg Pro Cys Thr Lys Cys Pro Gln Gly
            100                 105                 110
ATC CCT GTC CTC CAG GAA TGC AAC TCC ACA GCT AAC ACT GTG TGC AGT          479
Ile Pro Val Leu Gln Glu Cys Asn Ser Thr Ala Asn Thr Val Cys Ser
        115                 120                 125
TCA TCT GTT TCA AAT CCC AGA AAC TGG CTG TTC CTA CTG ATG CTA ATT          527
Ser Ser Val Ser Asn Pro Arg Asn Trp Leu Phe Leu Leu Met Leu Ile
    130                 135                 140
GTC TTC TGT ATC TGAAGAAGAT AAAGGTTCTA CAGATGGTGT CTGTAGCTTC              579
Val Phe Cys Ile
145
CTTTTATTGC TGTGAAGAGA AACCATGGAG GCAACTCTTT CATTTTATTT TATTTTTTAA        639
TGTCTTGAAC TTGATTTGAA GACCAGGCTG GACTCAAACT CACAGAGATC CGGACTAGGC        699
ACCTCTAATA TAGGAAAACA TTGAATTGGG ACTGGCTTAC AGTTTCAGAA GTTCTGTCCA        759
TGATTATCAT AGTGCGAAGC ATGGAGGCAC GGAGGCACAC ATGGTGCTGG AGAAGAAGCT        819
GAGAGTTCTG CATCTTGATC TGCAAGCAAT AAAAGGAGAC TGTGTGCCAC ACTACACATA        879
GCTTGAACAT AGGAGACCTC AAAGCCTGTC CCCACAGTGA CAAACTTCCT CCAACAAGGT        939
CATACCTCCT AATAATACCA TTTCTTATGA GGCAAGCATT CAAACACATG AGTCTATGAG        999
GGCCAAACCA ATTCAAACCA CCACAGGTTA ACAATTGCCC TCTGCAGCTC TCTGGTGGAG       1059
GCCCTCCTTG AGAGTAAGTA ACAATTTAGA TGAAGGCAAG TCCTGGTATC AGGTCCAAAA       1119
GAAACTCAGG ATGAATGGTC CACTGTGGTT CCTATTAACA TACTGAAGAA CATGACCTCA       1179
CCTTAGACTT CTCCACCTCA CTGGCTTCCC TTCCCCTAGC TTCTCATTCC CAGGTAACCC       1239
TGCCATTTTT TGGTAATGTG CCTTCTTGGT TCTTCCTCTC CTTTCCCCCT CTCTTCTGGT       1299
CCTTATTTCT CTTCCTCTCC CACTCTCCAC CAGCCGCCTC TTAAGGCCTG AGTCAGTCTG       1359
CAGGCCATGT TTAATCTACT ACTTTCTCTC TGCTCTGGAC TCATCCAGAT GTCTCTGGCT       1419
GAGCTCTCCC TCCTATCTAC AATAAAACCT TCCCCCTAAC CAGAAATGGA ACAGTTTTGT       1479
CCTCACTTTG TACATCTGGT GCCTGAAACC                                        1509
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SEQ ID NO: 4:

SEQUENCE LENGTH: 43
STRANDEDNESSS: single
TOPOLOGY: liner
MOLECULE TYPE: Other nucleic acid, synthetic DNA
SEQUENCE DENCRIPTION: SEQ ID NO: 4:
GCGGCCGCGA ATTCTGACTA ACTGACGGGG GGGGGGGGGG GGG 43

SEQ ID NO: 5:
SEQUENCE LENGTH: 26
STRANDEDNESSS: single
TOPOLOGY: liner
MOLECULE TYPE: Other nucleic acid, synthetic DNA
SEQUENCE DENCRIPTION: SEQ ID NO: 5:
CCGCGAGCTC GATATCAAGC TTGTAC 26

SEQ ID NO: 6:
SEQUENCE LENGTH: 29
STRANDEDNESSS: single
TOPOLOGY: liner
MOLECULE TYPE: Other nucleic acid, synthetic DNA
SEQUENCE DENCRIPTION: SEQ ID NO: 6:
GGCGCTCGAG CTATAGTTCG AACATGGAG 29

SEQ ID NO: 7:
SEQUENCE LENGTH: 29
STRANDEDNESSS: single
TOPOLOGY: liner
MOLECULE TYPE: Other nucleic acid, synthetic DNA
SEQUENCE DENCRIPTION: SEQ ID NO: 7:
GAGGTACAAG CTTGATATCG AGCTCGCGG 29

SEQ ID NO: 8:
SEQUENCE LENGTH: 23
STRANDEDNESSS: single
TOPOLOGY: liner
MOLECULE TYPE: Other nucleic acid, synthetic DNA

SEQUENCE DENCRIPTION: SEQ ID NO: 8:
GCCGCGAATT CTGACTAACT GAC 23

SEQ ID NO: 9:
SEQUENCE LENGTH: 24
STRANDEDNESSS: single
TOPOLOGY: liner
MOLECULE TYPE: Other nucleic acid, synthetic DNA
SEQUENCE DENCRIPTION: SEQ ID NO: 9:
GGATCCTTCA ACTGTCCCGA TGGT 24

SEQ ID NO: 10:
SEQUENCE LENGTH: 26
STRANDEDNESSS: single
TOPOLOGY: liner
MOLECULE TYPE: Other nucleic acid, synthetic DNA
SEQUENCE DENCRIPTION: SEQ ID NO: 10:
GAATTCCACA CAGTGTTAGC TGTGGA 26

SEQ ID NO: 11:
SEQUENCE LENGTH: 36
STRANDEDNESSS: single
TOPOLOGY: liner
MOLECULE TYPE: Other nucleic acid, synthetic DNA
SEQUENCE DENCRIPTION: SEQ ID NO: 11:
CCGAATTCCA CCATGGTTAC CTTCAGCCAC GTCTCC 36

SEQ ID NO: 12:
SEQUENCE LENGTH: 35
STRANDEDNESSS: single
TOPOLOGY: liner
MOLECULE TYPE: Other nucleic acid, synthetic DNA
SEQUENCE DENCRIPTION: SEQ ID NO: 12:
CCGGATCCTC AGATACAGAA GACAATTAGC ATCAG 35